



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 183002

TO: Chun Crowder
Location: REM-3B59/3C70
Art Unit: 1644
Monday, March 27, 2006

Case Serial Number: 10/644021

From: Deirdre Arnold
Location: Biotech-Chem Library
REM 1A55
Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

Search Notes

Please feel free to contact me if you have any questions or would like to amend the search.

Thank you for using STIC services.

Regards,
Deirdre Arnold



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Crowder, Chun

To: STIC-Biotech/ChemLib
Subject: Sequence search for 10/644,021

SEQ ID NO:2 against commercial and interference protein databases.
Thanks!

Chun Crowder, Ph.D.
81042
Patent Examiner
TC1644
Remsen/03B59
3c70
571-272-8142

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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 24, 2006, 16:42:20 ; Search time 187 Seconds
(Without alignments)
878.758 Million cell updates/sec

Title: US-10-644-021A-2

Perfect score: 1952
Sequence: 1 MEVVKCLGHEEFYRLVRR.....WQYLTLSQVTEEDYVGTGSH 374

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1952	100.0	374	6	ABG72689 Human squ
2	1952	100.0	374	8	ADN96862 Novel hum
3	1920.5	98.4	417	2	AAW01739 Human squ
4	1920.5	98.4	417	7	AD58269 Human pro
5	1920.5	98.4	417	7	ADDA6345 Human pro
6	1920.5	98.4	417	7	AD58261 Human pro
7	1920.5	98.4	417	7	AD58265 Human pro
8	1920.5	98.4	417	7	AD58273 Human pro
9	1920.5	98.4	417	7	ADJ94872 Novel NOV
10	1920.5	98.4	417	8	ADN96865 Farnesyl-
11	1920.5	98.4	417	8	ADN96864 Farnesyl-
12	1920.5	98.4	417	8	ADT79957 Human squ
13	1920.5	98.4	417	9	ADY16510 PRO polyp
14	1920.5	98.4	417	9	AD270390 Human pro
15	1915.5	98.1	417	2	AAK52606 Human squ
16	1915.5	98.1	417	8	ADN96866 Farnesyl-
17	1915.5	98.1	417	8	ADT79958 Human squ
18	1912.5	89.0	417	8	ADN96862 Human squ
19	1737	89.0	416	5	ABBS7061 Mouse lsc
20	1692	86.7	416	7	AD58271 Rat equal
21	1692	86.7	416	7	AD58271 Rat equal
22	1692	86.7	416	7	AD58259 Rat Prote
23	1692	86.7	416	7	AD58267 Rat Prote
24	1692	86.7	416	7	AD58263 Rat Prote

25	1568	80.3	358	8	ADH45289 Human enz
26	770.5	39.5	455	8	ADY11030 Plant ful
27	747.5	38.3	411	2	AAK94574 Squalene
28	744	38.1	460	2	AAW01738 S. pombe
29	744	38.1	460	2	ADN19728 Bacterial
30	735.5	37.7	428	8	ADY13030 Plant ful
31	732	37.5	404	8	ADT60095 Plant pol
32	731	37.4	404	3	AAK32432 Arabidops
33	731	37.4	404	3	AAK32431 Arabidops
34	731	37.4	410	3	AAK32431 Arabidops
35	731	37.4	410	3	AAK32431 Arabidops
36	723.5	37.4	410	7	ADG87340 Arabidops
37	723.5	37.1	448	5	ABP73518 Candida a
38	721	36.9	391	3	AAK32432 Arabidops
39	721	36.9	391	3	AAK32433 Arabidops
40	717.5	36.8	413	7	ADP89797 M. trunca
41	716.5	36.7	388	7	ADG87344 Arabidops
42	702	36.0	441	5	AAU11290 Ashbya go
43	695.5	35.6	528	6	ABJ26447 Aspergill
44	689.5	35.3	444	8	ADN96865 S. cerevi
45	688.5	35.3	444	7	ADK65639 S. cerevis

ALIGNMENTS

```
RESULT 1
ABG72689 standard; protein; 374 AA.
ID      ABG72689;
XX
AC      ABG72689;
XX
DT      05-MAR-2003 (first entry)
XX
DE      Human squalene synthase.
XX
KW      Human; enzyme; squalene synthase; cholesterol-related disease;
KW      cardiovascular disease; chromosome 8; SNP;
KW      single nucleotide polymorphism.
XX
OS      Homo sapiens.
XX
XX
XX      Location/Qualifiers
XX      Key
XX      MISC-difference 45
XX      FT      /note="May be Arg as a result of a single nucleotide
XX      FT      polymorphism"
XX
XX      US2002142418-A1.
XX
XX      PD      03-OCT-2002.
XX
XX      PF      29-MAR-2001; 2001US-00820004.
XX
XX      PR      29-MAR-2001; 2001US-00820004.
XX
XX      (WEIM/) WEI M.
XX      (YANC/) YAN C.
XX      (DFRA/) DI FRANCESCO V.
XX      (BEAS/) BEASLEY E M.
XX
XX      Wei M, Yan C, Di Francesco V, Beasley EM;
XX      WPI; 2003-155945/15.
XX      N-PSDB; ABX14651, ABX14652.
XX
XX      Novel isolated enzyme protein related to synthase enzyme subfamily,
XX      useful as models for developing human therapeutic targets, aid in the
XX      identification of therapeutic proteins and as immunogens to raise
XX      antibodies.
XX      Claim 1; Fig 2; 76pp; English.
XX
XX      The invention relates to an isolated enzyme protein (a squalene synthase)
```


PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-033347P.
XX
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
PI Woolf C, D'urso D, Befort K, Costigan M;
PI WPI; 2003-268312/26.
DR GENBANK; P37268.
PT
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
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XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
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CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC polynucleotide, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
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CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
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CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
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CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 417 AA:
SQ
Query Match 98.4%; Score 1920.5; DB 7; Length 417;
Best Local Similarity 89.7%; Pred. No. 6.1e-192;
Matches 374; Conservative 0; Mismatches 0; Indels 43; Gaps 1;
QY 1 MEPEKCGHPEEFNVLVFRIRGGRKMPKMDQDSSLSSTCKYKYNQTSRSPAAVIOA 60
DB 1 MEPEKCGHPEEFNVLVFRIRGGRKMPKMDQDSSLSSTCKYKYNQTSRSPAAVIOA 60
QY 61 LDGEMRAVAVCIFFYLALDTLEDMDTISEKKVPLLNHFSFLYQDPWFMSKEDKRD 120
DB 61 LDGEMRAVAVCIFFYLALDTLEDMDTISEKKVPLLNHFSFLYQDPWFMSKEDKRD 120
QY 121 VLEDEFT-----YCHVAVLGV 137
DB 121 VLEDEFT-----YCHVAVLGV 137
QY 121 VLEDEFT-----YCHVAVLGV 137
DB 121 VLEDEFT-----YCHVAVLGV 137
QY 138 IGSRLTSASGFEPDLYGDETERANSMLPLQKNTIRDYLEDQGGRETFPQWRSRYV 197
DB 138 IGSRLTSASGFEPDLYGDETERANSMLPLQKNTIRDYLEDQGGRETFPQWRSRYV 197
QY 181 IGSRLTSASGFEPDLYGDETERANSMLPLQKNTIRDYLEDQGGRETFPQWRSRYV 240
DB 181 IGSRLTSASGFEPDLYGDETERANSMLPLQKNTIRDYLEDQGGRETFPQWRSRYV 240
QY 198 KKLGDPKPEPIDAVOCNLNLTNALHHPDVTYTSRLRNSGVFFCAIPQWMAATL 257
DB 198 KKLGDPKPEPIDAVOCNLNLTNALHHPDVTYTSRLRNSGVFFCAIPQWMAATL 257
QY 241 KKLGDPKPEPIDAVOCNLNLTNALHHPDVTYTSRLRNSGVFFCAIPQWMAATL 300
DB 241 KKLGDPKPEPIDAVOCNLNLTNALHHPDVTYTSRLRNSGVFFCAIPQWMAATL 300
QY 258 AACTNNQOVFKGAVKIRKQAVTLMDATNMPAVKAIIOYMEBIYHRIPDSDPSSSKTR 317
DB 258 AACTNNQOVFKGAVKIRKQAVTLMDATNMPAVKAIIOYMEBIYHRIPDSDPSSSKTR 317

DB 301 AACTNNQOVFKGAVKIRKQAVTLMDATNMPAVKAIIOYMEBIYHRIPDSDPSSSKTR 360
QY 318 QIISTRTQNLNPNCOILSRSHYSPILYLFVWMLAALSWQYLTTLTSGVTEDDYQGTGEH 374
DB 361 QIISTRTQNLNPNCOILSRSHYSPILYLFVWMLAALSWQYLTTLTSGVTEDDYQGTGEH 417
RESULT 5
ADD46345
ID ADD46345 standard; protein; 417 AA.
XX
XX ADD46345;
XX
XX 29-JAN-2004 (first entry)
DT
DT Human Protein P37268, SEQ ID NO 12023.
DE
DE
XX Human; pain; neuronal tissue; gene therapy;
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
OS
XX
XX MO2003016475-A2.
PN
XX 27-FEB-2003.
PD
XX
XX 14-AUG-2002; 2002WO-US025765.
PF
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 14-AUG-2001; 2001US-0346382P.
PR 01-NOV-2001; 2001US-033347P.
PR 26-NOV-2001; 2001US-033347P.
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XX (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
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PI WPI; 2003-268312/26.
DR GENBANK; P37268.
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XX
XX
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CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
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CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
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SQ
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Best Local Similarity 89.7%; Pred. No. 6.1e-192;
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QY 1 MEVFKCGHPEEFNVLVRFIRIGKRRKMPKDDSSLSLTKCYKYNQTSRSPAAVIA 60
1 MEVFKCGHPEEFNVLVRFIRIGKRRKMPKDDSSLSLTKCYKYNQTSRSPAAVIA 60
DB 1 MEVFKCGHPEEFNVLVRFIRIGKRRKMPKDDSSLSLTKCYKYNQTSRSPAAVIA 60
QY 61 LDGEMRNAVCIFYLVLRALDLEDDMTISVEKKVPLIHNHSPFLYQPMRFMSKEDRQ 120
61 LDGEMRNAVCIFYLVLRALDLEDDMTISVEKKVPLIHNHSPFLYQPMRFMSKEDRQ 120
DB 61 LDGEMRNAVCIFYLVLRALDLEDDMTISVEKKVPLIHNHSPFLYQPMRFMSKEDRQ 120
QY 121 VLEDFPT-----YCHVAGLVG 137
121 VLEDFPTISLEFRLAEKQTVIADICRMGIGMAEFLDKHVTSEQEMDKYCHVAGLVG 180
DB 121 VLEDFPTISLEFRLAEKQTVIADICRMGIGMAEFLDKHVTSEQEMDKYCHVAGLVG 180
QY 138 IGLSRLFSASEFEDPLVGEDTERANSWGLFLOKNTIIRDTLEDOQGRFEPQVMSRYV 197
138 IGLSRLFSASEFEDPLVGEDTERANSWGLFLOKNTIIRDTLEDOQGRFEPQVMSRYV 197
DB 181 IGLSRLFSASEFEDPLVGEDTERANSWGLFLOKNTIIRDTLEDOQGRFEPQVMSRYV 240
QY 198 KKGDFAPKPNIDLAVOCLNELITNALHHPDVITYLSRLNOSVFNFCAIPQVMAIATL 257
198 KKGDFAPKPNIDLAVOCLNELITNALHHPDVITYLSRLNOSVFNFCAIPQVMAIATL 257
DB 241 KKGDFAPKPNIDLAVOCLNELITNALHHPDVITYLSRLNOSVFNFCAIPQVMAIATL 300
QY 258 AACYNNOQVFKGAVKIRKQAVTLMMDATMPAVKAIYYQMEIYHRIIPSDSSSKTR 317
258 AACYNNOQVFKGAVKIRKQAVTLMMDATMPAVKAIYYQMEIYHRIIPSDSSSKTR 317
DB 301 AACYNNOQVFKGAVKIRKQAVTLMMDATMPAVKAIYYQMEIYHRIIPSDSSSKTR 360
QY 318 QIISTIRTONLPNCQLISRSHPISPIYLSFWMLAALSMQYLTITTSQVTEDEVQGEH 374
318 QIISTIRTONLPNCQLISRSHPISPIYLSFWMLAALSMQYLTITTSQVTEDEVQGEH 374
DB 361 QIISTIRTONLPNCQLISRSHPISPIYLSFWMLAALSMQYLTITTSQVTEDEVQGEH 417
RESULT 6
ADES8261
ID ADE58261 standard; protein; 417 AA.
XX
AC ADE58261;
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P37268, SEQ ID NO 4132.
XX
DE Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urbo D, Befort K, Costigan M;
XX
DR WPI, 2003-268312/26.
XX
DR GENBANK, P37268.
XX
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CC the expression of a polynucleotide sequence which is differentially
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CC polynucleotides, a method for producing a pharmaceutical composition, a
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XX
SQ Sequence 417 AA;
Query Match 98.4%; Score 1920.5; DB 7; Length 417;
Best Local Similarity 89.7%; Pred. No. 6.1e-192;
Matches 374; Conservative 0; Mismatches 0; Indels 43; Gaps 1;
QY 1 MEVFKCGHPEEFNVLVRFIRIGKRRKMPKDDSSLSLTKCYKYNQTSRSPAAVIA 60
1 MEVFKCGHPEEFNVLVRFIRIGKRRKMPKDDSSLSLTKCYKYNQTSRSPAAVIA 60
DB 1 MEVFKCGHPEEFNVLVRFIRIGKRRKMPKDDSSLSLTKCYKYNQTSRSPAAVIA 60
QY 61 LDGEMRNAVCIFYLVLRALDLEDDMTISVEKKVPLIHNHSPFLYQPMRFMSKEDRQ 120
61 LDGEMRNAVCIFYLVLRALDLEDDMTISVEKKVPLIHNHSPFLYQPMRFMSKEDRQ 120
DB 61 LDGEMRNAVCIFYLVLRALDLEDDMTISVEKKVPLIHNHSPFLYQPMRFMSKEDRQ 120
QY 121 VLEDFPT-----YCHVAGLVG 137
121 VLEDFPTISLEFRLAEKQTVIADICRMGIGMAEFLDKHVTSEQEMDKYCHVAGLVG 180
DB 121 VLEDFPTISLEFRLAEKQTVIADICRMGIGMAEFLDKHVTSEQEMDKYCHVAGLVG 180
QY 138 IGLSRLFSASEFEDPLVGEDTERANSWGLFLOKNTIIRDTLEDOQGRFEPQVMSRYV 197
138 IGLSRLFSASEFEDPLVGEDTERANSWGLFLOKNTIIRDTLEDOQGRFEPQVMSRYV 197
DB 181 IGLSRLFSASEFEDPLVGEDTERANSWGLFLOKNTIIRDTLEDOQGRFEPQVMSRYV 240
QY 198 KKGDFAPKPNIDLAVOCLNELITNALHHPDVITYLSRLNOSVFNFCAIPQVMAIATL 257
198 KKGDFAPKPNIDLAVOCLNELITNALHHPDVITYLSRLNOSVFNFCAIPQVMAIATL 257
DB 241 KKGDFAPKPNIDLAVOCLNELITNALHHPDVITYLSRLNOSVFNFCAIPQVMAIATL 300
QY 258 AACYNNOQVFKGAVKIRKQAVTLMMDATMPAVKAIYYQMEIYHRIIPSDSSSKTR 317
258 AACYNNOQVFKGAVKIRKQAVTLMMDATMPAVKAIYYQMEIYHRIIPSDSSSKTR 317
DB 301 AACYNNOQVFKGAVKIRKQAVTLMMDATMPAVKAIYYQMEIYHRIIPSDSSSKTR 360
QY 318 QIISTIRTONLPNCQLISRSHPISPIYLSFWMLAALSMQYLTITTSQVTEDEVQGEH 374
318 QIISTIRTONLPNCQLISRSHPISPIYLSFWMLAALSMQYLTITTSQVTEDEVQGEH 374
DB 361 QIISTIRTONLPNCQLISRSHPISPIYLSFWMLAALSMQYLTITTSQVTEDEVQGEH 417
RESULT 7
ADES8265
ID ADE58265 standard; protein; 417 AA.
XX
AC ADE58265;
DT 29-JAN-2004 (first entry)
XX

DE Human Protein P37268, SEQ ID NO 4136.
XX Human; pain; neuronal tissue; gene therapy;
KM spinal segmental nerve injury; chronic constriction injury; CCI;
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XX MO2003016475-A2.
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QY 1 MEFAVKCLGHEEPEFYNLVFRIGGRKRWPKMDQDSSLSSLKTCYKYNQTSRSPAAYIQ 60
DB 1 MEFAVKCLGHEEPEFYNLVFRIGGRKRWPKMDQDSSLSSLKTCYKYNQTSRSPAAYIQ 60
QY 1 LDGEMRNAAVCTFYVLALDPTLEDMDTISVKKKPYLHNHFSFIYQDPMRMEKEKDRQ 120
DB 1 LDGEMRNAAVCTFYVLALDPTLEDMDTISVKKKPYLHNHFSFIYQDPMRMEKEKDRQ 120
QY 61 LDGEMRNAAVCTFYVLALDPTLEDMDTISVKKKPYLHNHFSFIYQDPMRMEKEKDRQ 120
DB 61 LDGEMRNAAVCTFYVLALDPTLEDMDTISVKKKPYLHNHFSFIYQDPMRMEKEKDRQ 120

QY 121 VLEDPT-----YCHYVAGLVG 137
DB 121 VLEDPTISLEBRNLAKEYQVIADI CRRMGI GMAEFLDKHVTSEQEMDKYCHYVAGLVG 180
QY 138 IGLSRIFSASEPFDPLVGEDTERANSMGLFLOKTNIRPYLEDQSGREFFWPEVMSRYV 197
DB 181 IGLSRIFSASEPFDPLVGEDTERANSMGLFLOKTNIRPYLEDQSGREFFWPEVMSRYV 240
QY 198 KKLGFAPKPEPIDLAVQCLNELITNALHHI PDVITYLSRLRQSVNFCALPQVMAIATL 257
DB 241 KKLGFAPKPEPIDLAVQCLNELITNALHHI PDVITYLSRLRQSVNFCALPQVMAIATL 300
QY 258 AACYNQOVFKGAVKTRKQAVTLMMDATMMPAVKAI IYQYMEIYHRI PDSPSSSKR 317
DB 301 AACYNQOVFKGAVKTRKQAVTLMMDATMMPAVKAI IYQYMEIYHRI PDSPSSSKR 360
QY 318 QITSTIRTONLPNCOLISRSHPYLSFVMLAALSMQYLTLSQVTEBDYVQTGEH 374
DB 361 QITSTIRTONLPNCOLISRSHPYLSFVMLAALSMQYLTLSQVTEBDYVQTGEH 417
RESULT 8
ADES8273
ID ADE58273 standard; protein; 417 AA.
XX
XX ADE58273;
AC XX
XX 29-JAN-2004 (first entry)
DT XX
DE Human Protein P37268, SEQ ID NO 4144.
XX
XX Human; pain; neuronal tissue; gene therapy;
KM spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.
OS Homo sapiens.
XX MO2003016475-A2.
PN 27-FEB-2003.
PD 14-AUG-2002; 2002MO-US025765.
PF 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; P37268.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PS Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX
 SQ Sequence 417 AA:

Query Match 98.4%; Score 1920.5; DB 7; Length 417;
 Best Local Similarity 89.7%; Pred. No. 6.1e-192;
 Matches 374; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

QY 1 MEFYKCIHQPEEFYVLRALDLEDDMTISVEKKYPLAHNFSELYQDPMRMESKEDRQ 60
 DB 1 MEFYKCIHQPEEFYVLRALDLEDDMTISVEKKYPLAHNFSELYQDPMRMESKEDRQ 60
 QY 61 LDGEMRNAVCIFYVLRALDLEDDMTISVEKKYPLAHNFSELYQDPMRMESKEDRQ 120
 DB 61 LDGEMRNAVCIFYVLRALDLEDDMTISVEKKYPLAHNFSELYQDPMRMESKEDRQ 120
 QY 121 VLEDFPFTISLEFNNLAERYQTVIADICRMGIGMAEFLDKAVTSQEDMDKCHVVAQLVG 180
 DB 121 VLEDFPFTISLEFNNLAERYQTVIADICRMGIGMAEFLDKAVTSQEDMDKCHVVAQLVG 180
 QY 138 IGLSRLTSASEFEDPLVGEDTERANSMGLFLQKTNIIIRDYLEDDQGGREFWPQEWRSYV 197
 DB 181 IGLSRLTSASEFEDPLVGEDTERANSMGLFLQKTNIIIRDYLEDDQGGREFWPQEWRSYV 240
 QY 198 KKLGDFAKPEINIDLAQCLNELITNALHHIPDIVITYISRLNSQVFNFCALPQWALATL 257
 DB 241 KKLGDFAKPEINIDLAQCLNELITNALHHIPDIVITYISRLNSQVFNFCALPQWALATL 300
 QY 258 AACNNNOQVFGAVKIRKGOAVLTMMDATNNPAKAIYYQMEETIYHRIIPSDSSSKTR 317
 DB 301 AACNNNOQVFGAVKIRKGOAVLTMMDATNNPAKAIYYQMEETIYHRIIPSDSSSKTR 360
 QY 318 QIISTIRTONLPNCOLISRSXSPYISFWMLAALSMQVYTTLSQVTEDEVQTCGEH 374
 DB 361 QIISTIRTONLPNCOLISRSXSPYISFWMLAALSMQVYTTLSQVTEDEVQTCGEH 417

RESULT 9
 ADJ94872
 ID ADJ94872 standard; protein; 417 AA.

XX
 AC ADJ94872;

DT 06-MAY-2004 (first entry)

XX
 DE Novel NOVX protein sequence #50.

XX antidiabetic; anorectic; cardiac; hypotensive; antiarteriosclerotic;
 KW anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic;
 KW neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;
 KW antiaesthetic; antiinflammatory; dermatological; antisthmatic;
 KW antileptic; gene therapy; metabolic disorder; diabetes; obesity;
 KW infectious disease; anorexia; cancer; cardiovascular disease;
 KW hypertension; atherosclerosis; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;
 KW osteoarthritis; hematopoietic disorder; inflammatory skin disorder;
 KW asthma; dyslipidemia; neurogenesis; cell differentiation;
 KW cell proliferation; hematopoiesis; wound healing; angiogenesis;
 KW chromosome mapping; tissue typing; pharmacogenomic.

OS Homo sapiens.

XX
 PN WO2003040325-A2.

XX
 PD 15-MAY-2003.

XX
 PF 05-NOV-2002; 2002WO-US035464.

PR 05-NOV-2001; 2001US-0338626P.
 PR 06-NOV-2001; 2001US-033072P.
 PR 09-NOV-2001; 2001US-034823P.
 PR 15-NOV-2001; 2001US-0335610P.
 PR 16-NOV-2001; 2001US-0338543P.
 PR 20-NOV-2001; 2001US-0331630P.
 PR 20-NOV-2001; 2001US-0331610P.
 PR 21-NOV-2001; 2001US-0332152P.
 PR 27-NOV-2001; 2001US-033461P.
 PR 28-NOV-2001; 2001US-0333912P.
 PR 28-NOV-2001; 2001US-0334027P.
 PR 29-NOV-2001; 2001US-0334300P.
 PR 30-NOV-2001; 2001US-0334421P.
 PR 30-NOV-2001; 2001US-0334526P.
 PR 04-DEC-2001; 2001US-0336576P.
 PR 04-DEC-2001; 2001US-033664P.
 PR 07-DEC-2001; 2001US-0338314P.
 PR 10-DEC-2001; 2001US-0338390P.
 PR 10-DEC-2001; 2001US-0339006P.
 PR 11-DEC-2001; 2001US-0339286P.
 PR 01-FEB-2002; 2002US-0353280P.
 PR 01-FEB-2002; 2002US-0353288P.
 PR 04-FEB-2002; 2002US-0354392P.
 PR 04-FEB-2002; 2002US-0354393P.
 PR 04-FEB-2002; 2002US-0354409P.
 PR 27-FEB-2002; 2002US-0359944P.
 PR 27-FEB-2002; 2002US-0360148P.
 PR 05-MAR-2002; 2002US-0361790P.
 PR 05-MAR-2002; 2002US-0361833P.
 PR 05-MAR-2002; 2002US-0361925P.
 PR 05-MAR-2002; 2002US-0362250P.
 PR 05-MAR-2002; 2002US-0362625P.
 PR 13-MAR-2002; 2002US-0364000P.
 PR 13-MAR-2002; 2002US-0364181P.
 PR 13-MAR-2002; 2002US-0364182P.
 PR 13-MAR-2002; 2002US-0364187P.
 PR 13-MAR-2002; 2002US-0364227P.
 PR 17-MAY-2002; 2002US-0381621P.
 PR 28-MAY-2002; 2002US-0383675P.
 PR 17-JUL-2002; 2002US-0396703P.
 PR 06-AUG-2002; 2002US-0401552P.
 PR 07-AUG-2002; 2002US-0401594P.
 PR 07-AUG-2002; 2002US-0401787P.
 PR 15-AUG-2002; 2002US-0403619P.
 PR 20-AUG-2002; 2002US-0404821P.
 PR 23-AUG-2002; 2002US-0405368P.
 PR 23-AUG-2002; 2002US-0405402P.
 PR 23-AUG-2002; 2002US-0405496P.
 PR 23-AUG-2002; 2002US-0405631P.
 PR 26-AUG-2002; 2002US-0406125P.
 PR 04-NOV-2002; 2002US-00287226.

XX (CUBA-) CUBAGEN CORP.

XX Agee ML, Albrock JP, Bergis C, Boldog FL, Burgess CE, Chant JS,
 PI Chaudhuri A, Dipipo VA, Edinger SR, Eilen A, Ellerman K,
 PI Gargoli EA, Gorman L, Gerlach VL, Ji W, Kekuda R, Khramtsov NV,
 PI Li L, Malyankar UM, MacDougall JR, Mezes PS, Miller CE, Millet I,
 PI Ooi CE, Ott T, Padigam M, Patturajan M, Rastrelli L, Rieger DK,
 PI Rothenberg ME, Shenoy SG, Spaderna SK, Spytek KA, Taupier RJ,
 PI Vernet GM, Zernusen BD, Zhong M;
 DR WPI; 2003-441551/41.
 DR N-PsDB; ADJ94871.

XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.

PS Claim 1; SEQ ID NO 100; 800bp; English.

XX The invention relates to novel isolated polypeptides, mature forms of
CC these, or a sequence that is at least 95 % identical to, or having one or
CC more conservative amino acid substitutions in the polypeptides. The
CC polypeptides, nucleic acid molecules and antibodies are useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease, preferably a NOVX-associated disorder. The nucleic acid
CC molecules, polypeptides and antibodies are useful for treating,
CC preventing or diagnosing diseases such as metabolic disorders, diabetes,
CC obesity, infectious diseases (viral, bacterial, fungal, helminthic, and
CC protozoal), anorexia, cancer, cardiovascular diseases (hypertension,
CC atherosclerosis), neurodegenerative disorders, Alzheimer's disease,
CC Parkinson's disease, epilepsy, immune disorders (osteoarthritis),
CC hematopoietic disorders, inflammatory skin disorders, asthma, and various
CC dyslipidemias. The nucleic acids and polypeptides may also be used as
CC targets for the identification of small molecules that modulate or
CC inhibit e.g. neurogenesis, cell differentiation, cell proliferation,
CC hematopoiesis, wound healing and angiogenesis, in gene therapy, in
CC generation of antibodies that bind immunospecifically to NOVX substances
CC for use in therapeutic or diagnostic methods. The nucleic acids are
CC further used as hybridization probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenetics. This sequence
CC corresponds to one of the NOVX polypeptides of the invention.

XX Sequence 417 AA;

Query Match 98.4%; Score 1920.5; DB 7; Length 417;
Best Local Similarity 89.7%; Pred. No. 6.1e-192;
Matches 374; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

QY 1 MEFVKGHPPEEFYLVRRIGGRKRVKMDQSSLSLKTCKYKLNQTSRSPFAVIOA 60
DB 1 MEFVKGHPPEEFYLVRRIGGRKRVKMDQSSLSLKTCKYKLNQTSRSPFAVIOA 60
QY 61 LDGEMRNAVCIFYLVRAIDLTLEDMTISVEKKVPLLNHFSLYOPDWRPFMSKEDKQ 120
DB 61 LDGEMRNAVCIFYLVRAIDLTLEDMTISVEKKVPLLNHFSLYOPDWRPFMSKEDKQ 120
QY 121 VLEDPFTISLEFRNLAEKYQTIVADICRMGIGMAEFLDKHVTSEQEMDKYCHYVAGLVG 180
DB 121 VLEDPFTISLEFRNLAEKYQTIVADICRMGIGMAEFLDKHVTSEQEMDKYCHYVAGLVG 180
QY 138 IGSRLFSASBEFEDPLVGEDTERANSGLFLOKTNIRYDLEDOQGRFEPWQSVSRVY 197
DB 181 IGSRLFSASBEFEDPLVGEDTERANSGLFLOKTNIRYDLEDOQGRFEPWQSVSRVY 240
QY 198 KKLGDFAKPNIDIAVOCLELITNALHHIPDVITYYSRLRNOSVFNFCAIPQMAIATL 257
DB 241 KKLGDFAKPNIDIAVOCLELITNALHHIPDVITYYSRLRNOSVFNFCAIPQMAIATL 300
QY 258 AACANNOOVKGAVKIRKQAVTLMMDATMMPAKAIYYQMEIYHRIIDSPSSSKTR 317
DB 301 AACANNOOVKGAVKIRKQAVTLMMDATMMPAKAIYYQMEIYHRIIDSPSSSKTR 360
QY 318 QIISTIRTONLPNCQLISRSRHSPIYLSFWMLLAALSMQYLITLTSQVTEDEVOTGEH 374
DB 361 QIISTIRTONLPNCQLISRSRHSPIYLSFWMLLAALSMQYLITLTSQVTEDEVOTGEH 417

RESULT 10
ADN96865
ID ADN96865 standard; protein; 417 AA.

XX AC ADN96865;
XX DT 26-AUG-2004 (first entry)

XX Farnesyl-disphosphate farnesyltransferase 1.
DE disease diagnosis; gene expression associated disorder; gene expression;
XX enzyme peptide; human; enzyme;
KM farnesyl-disphosphate farnesyltransferase 1.
XX

OS Homo sapiens.

PN US2004106179-A1.

XX 03-JUN-2004.

XX 20-AUG-2003; 2003US-00644021.

XX 29-MAR-2001; 2001US-00820004.

XX (APPL-) APPLERA CORP.

XX Wei M, Yan C, Di Francesco V, Beasley E;

XX WPI; 2004-419461/39.

PT New isolated enzyme proteins, useful for diagnosing or treating diseases
PT characterized by absence, inappropriate, or unwanted expression of the
PT protein, or as a reagent in assays for determining levels of protein in
PT biological sample.

XX Disclosure; SEQ ID NO 5; 76bp; English.

XX The invention describes an isolated enzyme peptide (I) comprising a
CC defined sequence of 374 amino acids. Also described are: an isolated
CC antibody that selectively binds to (I); a method for producing the
CC peptide; a method for detecting the presence of the peptide; a method
CC for identifying a modulator of the peptide; a method for identifying an
CC agent that binds to the peptide; a pharmaceutical composition comprising
CC an agent identified by the method of (I) and a pharmaceutical carrier; a
CC method for treating a disease or condition mediated by a human enzyme
CC protein; a method for identifying a modulator of the expression of the
CC peptide; and an isolated human enzyme peptide having an amino acid
CC sequence that shares at least 70-90% homology with SEQ ID NO. 2.

CC Specifically claimed is an enzyme peptide comprising 374 amino acids (SRQ
CC ID NO. 2). The peptides are useful for substantial or specific assays,
CC e.g. biological, or drug screening assays; as a reagent in assays for
CC determining levels of protein in biological sample; and as markers for
CC tissues where the corresponding protein is expressed. It can also be used
CC to screen a compound for the ability to stimulate or inhibit interaction
CC between the enzyme protein and a molecule that normally interacts with
CC the enzyme protein. They are also useful as a target for diagnosing a
CC disease or predisposition to disease mediated by the peptide. It can also
CC be used for treating disorders characterized by absence, inappropriate,
CC or unwanted expression of the protein. This is the amino acid sequence
CC human farnesyl-disphosphate farnesyltransferase 1 used in a sequence
CC comparison with the novel human enzyme of the invention.

XX Sequence 417 AA;

Query Match 98.4%; Score 1920.5; DB 8; Length 417;
Best Local Similarity 89.7%; Pred. No. 6.1e-192;
Matches 374; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

QY 1 MEFVKGHPPEEFYLVRRIGGRKRVKMDQSSLSLKTCKYKLNQTSRSPFAVIOA 60

DB 1 MEFVKGHPPEEFYLVRRIGGRKRVKMDQSSLSLKTCKYKLNQTSRSPFAVIOA 60

QY 61 LDGEMRNAVCIFYLVRAIDLTLEDMTISVEKKVPLLNHFSLYOPDWRPFMSKEDKQ 120

DB 61 LDGEMRNAVCIFYLVRAIDLTLEDMTISVEKKVPLLNHFSLYOPDWRPFMSKEDKQ 120

QY 121 VLEDPFTISLEFRNLAEKYQTIVADICRMGIGMAEFLDKHVTSEQEMDKYCHYVAGLVG 137

DB 121 VLEDPFTISLEFRNLAEKYQTIVADICRMGIGMAEFLDKHVTSEQEMDKYCHYVAGLVG 180

PT New oligonucleotide targeted to a nucleic acid molecule encoding squalene
PT synthase, useful in diagnosing and treating atherosclerosis.
XX
PS Disclosure; Page 23-24; 67pp; English.
XX
CC The invention relates to a new compound 8-80 nucleobases in length (an
CC antiense oligonucleotide) targeted to a nucleic acid molecule encoding
CC squalene synthase (also known as farnesyl diphosphate farnesyl
CC transferase 1), where the compound specifically hybridizes with the
CC nucleic acid molecule encoding human squalene synthase appearing as
CC AD779915 and inhibits the expression of squalene synthase. Also included
CC are inhibiting the expression of squalene synthase in cells or tissues,
CC screening for a modulator of squalene synthase, a diagnostic method for
CC identifying a disease state, a kit or assay device comprising the
CC compound and treating an animal having a disease or condition associated
CC with squalene synthase. The compound and methods are useful in diagnosing
CC and treating disorders related to cholesterol biosynthesis e.g.
CC atherosclerosis, coronary heart disease and hypercholesterolaemia . The
CC present sequence is a squalene synthase protein sequence.
XX
SQ Sequence 417 AA;
XX
Query Match 98.4%; Score 1920.5; DB 8; Length 417;
Best Local Similarity 89.7%; Pred. No. 6.1e-192;
Matches 374; Conservative 0; Mismatches 0; Indels 43; Gaps 1;
XX
QY 1 MEFVKGHEEPEFNLVRRFRIGGRKRYMPKMDQSSLSSTKCYKYNQTSRSPAIVQA 60
Db 1 MEFVKCLGHPEEFNLVRRFRIGGRKRYMPKMDQSSLSSTKCYKYNQTSRSPAIVQA 60
XX
QY 61 LDGEMRNAVCIFYLVLRALDLEDDMTISVEKKVPLLNHFSFLYOPDMRFMESKEKDRQ 120
Db 61 LDGEMRNAVCIFYLVLRALDLEDDMTISVEKKVPLLNHFSFLYOPDMRFMESKEKDRQ 120
XX
QY 121 VLDEPPT-----YCHYVAGLVG 137
Db 121 VLDEPPTISLEFENLAEKRYQTIVADICRRMGIGMAEFLDKHVTSEQEMDKYCHYVAGLVG 180
XX
QY 138 IGLSRIFSASEFEDPLVGEDTERANSGLFLQKTNIIIRDYLEDOQGREFWPOEWSRYV 197
Db 181 IGLSRIFSASEFEDPLVGEDTERANSGLFLQKTNIIIRDYLEDOQGREFWPOEWSRYV 240
XX
QY 198 KKLGDFAKPEPIDLAVQCLNELITNALHHI PDVITYLSRLNQS VNFCAIPQVMAIATL 257
Db 241 KKLGDFAKPEPIDLAVQCLNELITNALHHI PDVITYLSRLNQS VNFCAIPQVMAIATL 300
XX
QY 258 AACYNNQOVFKGAVKIRKQAVTLMMDATNMPAVKAIITYQMEIYHRI PDSPSSSKTR 317
Db 301 AACYNNQOVFKGAVKIRKQAVTLMMDATNMPAVKAIITYQMEIYHRI PDSPSSSKTR 360
XX
QY 318 QIISTIRTONLPNCOLISRSYSPYLSFVWLAAALSMQYLTTLTSSQVTEDEVOTGEH 374
Db 361 QIISTIRTONLPNCOLISRSYSPYLSFVWLAAALSMQYLTTLTSSQVTEDEVOTGEH 417
XX
RESULT 13
ADY16510
ID ADY16510 standard; protein; 417 AA.
XX
AC ADY16510;
XX
DT 05-MAY-2005 (first entry)
XX
DE PRO polypeptide SEQ ID NO 2316.
XX
KW Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
KW Antiirreumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
KW Antithyroid; Antidiabetic; Nephrotoxic; CNS-Gen.; Hepatocytotoxic;
KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
KW Antiallergic; de; gene; diagnosis.
XX
XX Homo sapiens.
OS
XX

PN WO2005016962-A2.
XX
PD 24-FEB-2005.
XX
PF 11-AUG-2004; 2004WO-US026249.
XX
PR 11-AUG-2003; 2003US-0493546P.
XX
XX (GETH) GENENTECH INC.
XX
PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
PI WPI; 2005-182330/19.
XX
DR
XX
PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX
PS Claim 8; SEQ ID NO 2316; 158pp; English.
XX
XX
CC The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a DNA encoding a PRO
CC polypeptide.
XX
SQ Sequence 417 AA;
XX
Query Match 98.4%; Score 1920.5; DB 9; Length 417;
Best Local Similarity 89.7%; Pred. No. 6.1e-192;
Matches 374; Conservative 0; Mismatches 0; Indels 43; Gaps 1;
XX
QY 1 MEFVKGHEEPEFNLVRRFRIGGRKRYMPKMDQSSLSSTKCYKYNQTSRSPAIVQA 60
Db 1 MEFVKCLGHPEEFNLVRRFRIGGRKRYMPKMDQSSLSSTKCYKYNQTSRSPAIVQA 60
XX
QY 61 LDGEMRNAVCIFYLVLRALDLEDDMTISVEKKVPLLNHFSFLYOPDMRFMESKEKDRQ 120
Db 61 LDGEMRNAVCIFYLVLRALDLEDDMTISVEKKVPLLNHFSFLYOPDMRFMESKEKDRQ 120
XX
QY 121 VLDEPPT-----YCHYVAGLVG 137
Db 121 VLDEPPTISLEFENLAEKRYQTIVADICRRMGIGMAEFLDKHVTSEQEMDKYCHYVAGLVG 180
XX
QY 138 IGLSRIFSASEFEDPLVGEDTERANSGLFLQKTNIIIRDYLEDOQGREFWPOEWSRYV 197
Db 181 IGLSRIFSASEFEDPLVGEDTERANSGLFLQKTNIIIRDYLEDOQGREFWPOEWSRYV 240
XX
QY 198 KKLGDFAKPEPIDLAVQCLNELITNALHHI PDVITYLSRLNQS VNFCAIPQVMAIATL 257
Db 241 KKLGDFAKPEPIDLAVQCLNELITNALHHI PDVITYLSRLNQS VNFCAIPQVMAIATL 300
XX
QY 258 AACYNNQOVFKGAVKIRKQAVTLMMDATNMPAVKAIITYQMEIYHRI PDSPSSSKTR 317
Db 301 AACYNNQOVFKGAVKIRKQAVTLMMDATNMPAVKAIITYQMEIYHRI PDSPSSSKTR 360
XX
QY 318 QIISTIRTONLPNCOLISRSYSPYLSFVWLAAALSMQYLTTLTSSQVTEDEVOTGEH 374
Db 361 QIISTIRTONLPNCOLISRSYSPYLSFVWLAAALSMQYLTTLTSSQVTEDEVOTGEH 417
XX
RESULT 14
ADZ70390
ID ADZ70390 standard; protein; 417 AA.
XX
AC ADZ70390;
XX
DT 30-JUN-2005 (first entry)
XX
DE Human protein from lung cancer marker gene PDLT1.
XX
KW Tumor marker; lung tumor; cytostatic; neoplasia; expression;
KW

Db 181 IGLSRLFSASEFEDPLVGEDTERANSWGLFLOKTNIIIRDYLEDOQGGRFPWPQVWSRYV 240
QY 198 KXIGDFAKPENIDPLAVOCLNELITNALHHI PDVTTYLSRLNOSVFNFCAI PVMMAIATL 257
Db 241 KXIGDFAKPENIDPLAVOCLNELITNALHHI PDVTTYLSRLNOSVFNFCAI PVMMAIATL 300
QY 258 AACYNNOQVFKGAVKIRKGQAVTLMMDATNMPAVKAI IYQYMEIYHRIPDSDPSSKTR 317
Db 301 AACYNNOQVFKGAVKIRKGQAVTLMMDATNMPAVKAI IYQYMEIYHRIPDSDPSSKTR 360
QY 318 QIISTIRTONLPNCOLISRSHSPFIYLSFVMLAALSWOYLTTISQYTEDYVQTGEH 374
Db 361 QIISTIRTONLPNCOLISRSHSPFIYLSFVMLAALSWOYLTTISQYTEDYVQTGEH 417

Search completed: March 24, 2006, 16:45:49
Job time : 190 secs

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OM protein - protein search, using sw model

Run on: March 24, 2006, 16:50:05 ; Search time 46 Seconds
(Without alignments)
672.189 Million cell updates/sec

Title: US-10-644-021A-2

Sequence score: 1952
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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1952	100.0	374	2	US-09-820-004-2
2	1920.5	98.4	417	1	US-08-351-981-6
3	1920.5	98.4	417	2	US-09-820-004-4
4	1920.5	98.4	417	2	US-09-820-004-5
5	1920.5	98.4	417	2	US-09-949-016-6503
6	1920.5	98.4	436	2	US-09-949-016-11624
7	1915.5	98.1	417	2	US-09-820-004-6
8	1914.5	98.1	417	1	US-08-351-981-7
9	747.5	38.3	411	1	US-08-310-693-2
10	747.5	38.3	411	4	PCT-US95-11280-2
11	744	38.1	460	1	US-08-351-981-4
12	735	37.7	460	1	US-08-351-981-9
13	707.5	36.2	406	2	US-09-248-796A-17915
14	702	36.0	441	2	US-09-625-188-4
15	686.5	35.2	444	1	US-08-351-981-2
16	686.5	35.2	444	1	US-08-351-981-8
17	661	33.9	129	2	US-09-513-999C-5450
18	477	24.4	122	2	US-09-949-016-8257
19	181	9.3	296	1	US-07-783-705A-5
20	138.5	7.1	309	1	US-08-331-004A-2
21	138.5	7.1	309	4	PCT-US95-13937A-2
22	130	6.7	308	1	US-08-095-726-6
23	130	6.7	308	1	US-08-096-043-6
24	130	6.7	308	1	US-08-093-577-6
25	130	6.7	308	1	US-08-096-623A-6
26	130	6.7	308	2	US-10-808-807-10
27	119	6.1	303	2	US-08-660-645A-3

28	119	6.1	303	2	US-09-298-718-3	Sequence 3, Appl1
29	119	6.1	303	2	US-09-546-969-3	Sequence 3, Appl1
30	119	6.1	303	2	US-08-980-832-3	Sequence 6, Appl1
31	119	6.1	303	2	US-09-547-267-3	Sequence 3, Appl1
32	119	6.1	303	2	US-09-920-923B-3	Sequence 3, Appl1
33	116	5.9	410	2	US-09-691-270A-28	Sequence 26, Appl1
34	115.5	5.9	410	1	US-08-579-667-8	Sequence 8, Appl1
35	115	5.9	400	2	US-09-691-270A-14	Sequence 14, Appl1
36	114.5	5.9	413	1	US-08-579-667-4	Sequence 4, Appl1
37	113.5	5.8	410	1	US-08-579-667-2	Sequence 2, Appl1
38	111	5.7	402	2	US-09-180-342-3	Sequence 3, Appl1
39	111	5.7	412	2	US-09-371-307-76	Sequence 76, Appl1
40	109.5	5.6	410	1	US-08-579-667-6	Sequence 6, Appl1
41	109	5.6	252	2	US-09-691-270A-12	Sequence 12, Appl1
42	108	5.5	281	2	US-09-902-540-12624	Sequence 12624, A
43	107	5.5	310	2	US-09-691-270A-27	Sequence 27, Appl1
44	103	5.3	186	2	US-09-691-270A-4	Sequence 4, Appl1
45	102	5.2	408	2	US-09-691-270A-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-820-004-2
Sequence 2, Application US/09820004
Patent No. 6649385
GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THERMOF
FILE REFERENCE: C1001201
CURRENT APPLICATION NUMBER: US/09/820,004
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 374
TYPE: PRT
ORGANISM: Human
US-09-820-004-2

Query Match	100.0%	Score 1952	DB 2	Length 374
Best Local Similarity	100.0%	Pred. No. 9.5e-201		
Matches 374	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MEVFKCLGHPPEFYNLVRRRIGKKRKPMDODSLSSLTCTCYKYNQTSRSPFAVIOA	60	
DB	1	MEVFKCLGHPPEFYNLVRRRIGKKRKPMDODSLSSLTCTCYKYNQTSRSPFAVIOA	60	
QY	61	LDGEMRNACVIFYLVRLADLTEDMTISVEKVPDLNHFSPFYQPMWRMESKEKRO	120	
DB	61	LDGEMRNACVIFYLVRLADLTEDMTISVEKVPDLNHFSPFYQPMWRMESKEKRO	120	
QY	121	VLEDPTTYHYAGVIGLSTLFSASRPEDVLEDTERANSWGLFLQKTNIRDYLED	180	
DB	121	VLEDPTTYHYAGVIGLSTLFSASRPEDVLEDTERANSWGLFLQKTNIRDYLED	180	
QY	181	QOGRFQFQWRSRVKLGDFAPKPNIDLAQCLNELITNALHPIDVITYISRLNQ	240	
DB	181	QOGRFQFQWRSRVKLGDFAPKPNIDLAQCLNELITNALHPIDVITYISRLNQ	240	
QY	241	SVFNFCALPQWALATLAAQYNNQVFKGAVIRKQAVTLMQDATNMPAYKAIITYQME	300	
DB	241	SVFNFCALPQWALATLAAQYNNQVFKGAVIRKQAVTLMQDATNMPAYKAIITYQME	300	
QY	301	EYHRIIPDSDPSSSKTROISTITRONLPNCOLISHSYSPITYLSFWMLAALSQVYLT	360	
DB	301	EYHRIIPDSDPSSSKTROISTITRONLPNCOLISHSYSPITYLSFWMLAALSQVYLT	360	
QY	361	LSQVTEYVQTGEH 374		

DB 361 LSGQVTEDEVQGTGEH 374

RESULT 2

US-08-351-981-6
Sequence 6, Application US/08351981
Patent No. 5589372
GENERAL INFORMATION:
APPLICANT: Robinson, Gordon W.
TITLE OF INVENTION: Squalene Synthetase
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burton Rodney
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,981
FILING DATE:
CLASSIFICATION: 435
Prior Application DATA:
APPLICATION NUMBER: US/07/911,835
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gaul, Timothy J.
REGISTRATION NUMBER: 33,111
REFERENCE/DOCKET NUMBER: DC7a
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 252-4526
TELEFAX: (609) 252-4526
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-351-981-6

Query Match 98.4%; Score 1920.5; DB 1; Length 417;
Best Local Similarity 89.7%; Pred. No. 2.7e-197;
Matches 374; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

QY 1 MEVFKCLGHEEFYNNLVFRFIRGKRVKMPKMODSLSSSLKTCYKYNQTSRSPAIVIA 60
DB 1 MEVFKCLGHEEFYNNLVFRFIRGKRVKMPKMODSLSSSLKTCYKYNQTSRSPAIVIA 60
QY 61 LDGEMRNAVCIFYLVLRALDTELDMTISVEKKVPLLNHFHSLYQPDWRFMESKSKDRQ 120
DB 61 LDGEMRNAVCIFYLVLRALDTELDMTISVEKKVPLLNHFHSLYQPDWRFMESKSKDRQ 120
QY 121 VLEDPFTSLSEFNNLAKEYQTVIADICRMWIGMAEFLDKHVTSEQEMDKYCHYVAGLVG 137
DB 121 VLEDPFTSLSEFNNLAKEYQTVIADICRMWIGMAEFLDKHVTSEQEMDKYCHYVAGLVG 180
QY 138 IGLSRFLSASEFEDPLVGEDETERANSGLFLOKTNIIIRDYLEDOQGREGFWPQWWSRYV 197
DB 181 IGLSRFLSASEFEDPLVGEDETERANSGLFLOKTNIIIRDYLEDOQGREGFWPQWWSRYV 240
QY 198 KKLGDFAKPEPIDLAOCNELITNLAHLHPDVTYTLRLNOSVFNFCALPQWMAIATL 257
DB 241 KKLGDFAKPEPIDLAOCNELITNLAHLHPDVTYTLRLNOSVFNFCALPQWMAIATL 300
QY 258 AACYNNOQVFKGAVKIRKGOAVTLMMDATNMPAVKAIYQYMEIYHRIIPSDPSSSKTR 317
DB 301 AACYNNOQVFKGAVKIRKGOAVTLMMDATNMPAVKAIYQYMEIYHRIIPSDPSSSKTR 360

QY 318 QIISTIRTONLPNCOLISRSRHSPIYLSFVMLLAALSMQYLTTLTSGVTEDEVQGTGEH 374
DB 361 QIISTIRTONLPNCOLISRSRHSPIYLSFVMLLAALSMQYLTTLTSGVTEDEVQGTGEH 417

RESULT 3

US-09-820-004-4
Sequence 4, Application US/09820004
Patent No. 6649385
GENERAL INFORMATION:
APPLICANT: Mei, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
FILE REFERENCE: CL001201
CURRENT APPLICATION NUMBER: US/09/820,004
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 417
TYPE: PRT
ORGANISM: Human
US-09-820-004-4

Query Match 98.4%; Score 1920.5; DB 2; Length 417;
Best Local Similarity 89.7%; Pred. No. 2.7e-197;
Matches 374; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

QY 1 MEVFKCLGHEEFYNNLVFRFIRGKRVKMPKMODSLSSSLKTCYKYNQTSRSPAIVIA 60
DB 1 MEVFKCLGHEEFYNNLVFRFIRGKRVKMPKMODSLSSSLKTCYKYNQTSRSPAIVIA 60
QY 61 LDGEMRNAVCIFYLVLRALDTELDMTISVEKKVPLLNHFHSLYQPDWRFMESKSKDRQ 120
DB 61 LDGEMRNAVCIFYLVLRALDTELDMTISVEKKVPLLNHFHSLYQPDWRFMESKSKDRQ 120
QY 121 VLEDPFTSLSEFNNLAKEYQTVIADICRMWIGMAEFLDKHVTSEQEMDKYCHYVAGLVG 137
DB 121 VLEDPFTSLSEFNNLAKEYQTVIADICRMWIGMAEFLDKHVTSEQEMDKYCHYVAGLVG 180
QY 138 IGLSRFLSASEFEDPLVGEDETERANSGLFLOKTNIIIRDYLEDOQGREGFWPQWWSRYV 197
DB 181 IGLSRFLSASEFEDPLVGEDETERANSGLFLOKTNIIIRDYLEDOQGREGFWPQWWSRYV 240
QY 198 KKLGDFAKPEPIDLAOCNELITNLAHLHPDVTYTLRLNOSVFNFCALPQWMAIATL 257
DB 241 KKLGDFAKPEPIDLAOCNELITNLAHLHPDVTYTLRLNOSVFNFCALPQWMAIATL 300
QY 258 AACYNNOQVFKGAVKIRKGOAVTLMMDATNMPAVKAIYQYMEIYHRIIPSDPSSSKTR 317
DB 301 AACYNNOQVFKGAVKIRKGOAVTLMMDATNMPAVKAIYQYMEIYHRIIPSDPSSSKTR 360
QY 318 QIISTIRTONLPNCOLISRSRHSPIYLSFVMLLAALSMQYLTTLTSGVTEDEVQGTGEH 374
DB 361 QIISTIRTONLPNCOLISRSRHSPIYLSFVMLLAALSMQYLTTLTSGVTEDEVQGTGEH 417

RESULT 4

US-09-820-004-5
Sequence 5, Application US/09820004
Patent No. 6649385
GENERAL INFORMATION:
APPLICANT: Mei, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
FILE REFERENCE: CL001201
CURRENT APPLICATION NUMBER: US/09/820,004
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 24, 2006, 16:42:50 ; Search time 233 Seconds
(without alignments)

1132.479 Million cell updates/sec

Title: US-10-644-021A-2

Perfect score: 1952
Sequence: 1 MEFPVKLGHEEFYNLVRRF.....WQYLTLSQVTEEDYVGTGHH 374

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Uniprotc_05.80: *
1: uniprotc_sprotc: *
2: uniprotc_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1920.5	98.4	1 FDFI_HUMAN	P37268 homo sapien
2	1920.5	98.4	1 FDFI_HUMAN	Q61AXI homo sapien
3	1920.5	98.4	2 OSRGU_PONPY	Q516U3 pongo pygma
4	1820.5	93.3	4 O61E76_BOVIN	Q516U3 bos taurus
5	1737	89.0	1 FDFI_MOUSE	P53798 mus musculu
6	1737	89.0	1 FDFI_MOUSE	Q8BPF5 mus musculu
7	1692	86.7	1 FDFI_RAT	Q02769 ratuus norv
8	1527	78.2	1 FDFI_CHICK	Q52KWI gallus gall
9	1507.5	77.2	2 OSRGU_MOUSE	Q9GYU0 mus musculu
10	1208.5	61.9	2 OSRGU_MOUSE	Q4RRT3 tetradon n
11	755	38.7	2 OSRGU_MOUSE	Q52266 centella as
12	754	38.6	2 OSRGU_MOUSE	Q54DRI dictyosteli
13	753.5	38.6	2 OSRGU_MOUSE	Q54DRI dictyosteli
14	749.5	38.4	2 OSRGU_MOUSE	Q54DRI dictyosteli
15	746.5	38.2	1 FDFI_MOUSE	Q54DRI dictyosteli
16	744	38.1	1 FDFI_MOUSE	Q54DRI dictyosteli
17	737.5	37.8	2 OSRGU_MOUSE	Q54DRI dictyosteli
18	737.5	37.8	2 OSRGU_MOUSE	Q54DRI dictyosteli
19	737.5	37.8	2 OSRGU_MOUSE	Q54DRI dictyosteli
20	736	37.7	2 OSRGU_MOUSE	Q54DRI dictyosteli
21	735.5	37.7	2 OSRGU_MOUSE	Q54DRI dictyosteli
22	735.5	37.7	2 OSRGU_MOUSE	Q54DRI dictyosteli
23	732	37.5	2 OSRGU_MOUSE	Q54DRI dictyosteli
24	731.5	37.5	2 OSRGU_MOUSE	Q54DRI dictyosteli
25	731	37.4	2 OSRGU_MOUSE	Q54DRI dictyosteli
26	729.5	37.4	2 OSRGU_MOUSE	Q54DRI dictyosteli
27	729	37.3	2 OSRGU_MOUSE	Q54DRI dictyosteli
28	725.5	37.2	2 OSRGU_MOUSE	Q54DRI dictyosteli
29	723.5	37.1	2 OSRGU_MOUSE	Q54DRI dictyosteli
30	723.5	37.1	2 OSRGU_MOUSE	Q54DRI dictyosteli
31	721.5	37.0	2 OSRGU_MOUSE	Q54DRI dictyosteli

ALIGNMENTS

RESULT 1	ALIGNMENTS
32 720.5 36.9 413 2 Q42760 GLYGL	Q42760 glycyrhiza
33 717.5 36.8 413 2 Q6GSL6 MEDTR	Q6GSL6 medicago tr
34 714.5 36.6 418 2 Q9FUK1 ARTEMISIA	Q9FUK1 artemisia a
35 711.5 36.4 387 2 Q506K2 DARTIN	Q506K2 datura imo
36 711.5 36.4 410 2 Q62368 ORYSA	Q62368 oryza sativ
37 704.5 36.4 443 1 FDFI_PICUA	074165 picula jadi
38 702 36.0 441 1 FDFI_PICUA	Q752X9 ashbya gos
39 700.5 35.9 441 1 FDFI_PICUA	Q9H246 candida gla
40 699.5 35.8 471 2 Q4NAG4 ASPFU	Q4NAG4 aspergillus
41 693.5 35.5 693 2 Q5B7V4 EMENTI	Q5B7V4 aspergillus
42 688.5 35.3 444 1 FDFI_YEAST	P29704 saccharomyc
43 684.5 35.1 445 2 Q4P689 USTMA	Q4P689 ustilaago ma
44 683 35.0 445 1 FDFI_YEAST	Q9Y753 yarrowia li
45 680.5 34.9 572 1 FDFI_USTMA	Q92459 ustilaago ma

RESULT 1	ALIGNMENTS
1 FDFI_HUMAN	STANDARD; PRT; 417 AA.
AC P37268; Q96GT0;	
DT 01-OCT-1994 (Rel. 30, Created)	
DT 01-OCT-1994 (Rel. 30, Last sequence update)	
DT 10-MAY-2005 (Rel. 47, Last annotation update)	
DE Farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) (Squalene synthetase) (SS) (FPP: FPP farnesyltransferase).	
OS Name=FDFI1;	
GN Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;	
OC Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RA MEDLINE=93233634; PubMed=8474436;	
RA Robinson G.W., Teasy Y.H., Kienzie B.K., Smith-Monroy C.A.,	
RA Bishop R.W.;	
RT "Conservation between human and fungal squalene synthetases: similarities in structure, function, and regulation.";	
RL Mol. Cell. Biol. 13:2706-2727(1993).	
RL [2]	
RP NUCLEOTIDE SEQUENCE.	
RA TISSUE=Liver;	
RA MEDLINE=9122996; PubMed=7685352;	
RA Jiang G., McKenzie T.L., Conrad D.G., Shechter I.;	
RT "Transcriptional regulation by lovastatin and 25-hydroxycholesterol in HepG2 cells and molecular cloning and expression of the cDNA for the human hepatic squalene synthase.";	
RL J. Biol. Chem. 268:12818-12824(1993).	
RL [3]	
RP NUCLEOTIDE SEQUENCE.	
RA TISSUE=Liver;	
RA MEDLINE=9122996; PubMed=8294001; DOI=10.1016/0378-1119(93)90462-C;	
RA Sumners C., Karet F., Charles A.D.;	
RT "Cloning, expression and characterization of the cDNA encoding human hepatic squalene synthase, and its relationship to phytoene synthase.";	
RL Gene 136:185-192(1993).	
RL [4]	
RP NUCLEOTIDE SEQUENCE.	
RA TISSUE=Liver;	
RA MEDLINE=95168856; PubMed=7864626; DOI=10.1006/abbi.1995.1095;	
RA Solis D.A., McMahon G., Caplan S.L., Dudas D.A., Chamberlain H.A.,	
RA Velay A., Dottavio D., Rucker M.L., Engstrom R.G.,	
RA Cornell-Kennon S.A.;	
RT "Expression, purification, and characterization of the human squalene synthase: use of yeast and baculoviral systems.";	
RL Arch. Biochem. Biophys. 316:713-723(1995).	
RL [5]	
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT ARG-45.	
RA TISSUE=Lung, Muscle, and Urinary bladder;	

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Collins D.E., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Krausberg R.D., Collins D.E., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marishta K., Farmer A.A., Rubin G.M., Hong L.,
 RA Appleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Ricjards S., Wotley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Jakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallue D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."/
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6]
 X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 39-370.
 RA PubMed=10896663; DOI=10.1074/jbc.M00413200;
 RA Pandit J., Danley D.E., Schulte G.K., Mazzalupo S., Pauly T.A.,
 RA Hayward C.M., Hamanaka E.S., Thompson J.F., Harwood H.J. Jr.,
 RT "Crystal structure of human squalene synthase. A key enzyme in
 RT cholesterol biosynthesis."/
 J. Biol. Chem. 275:30610-30617(2000).
 CC -1- CATALYTIC ACTIVITY: 2 farnesyl diphosphate = diphosphate +
 CC presqualene diphosphate.
 CC -1- CATALYTIC ACTIVITY: Presqualene diphosphate + NADPH = diphosphate
 CC + squalene + NADP(+).
 CC -1- COFACTOR: Magnesium.
 CC -1- PATHWAY: Critical branch point enzyme of isoprenoid and
 CC cholesterol biosynthesis.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum.
 CC -1- SIMILARITY: Belongs to the phytoene/squalene synthetase family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; L06070; AAA60582.1; -; mRNA.
 DR EMBL; L06105; AAA36645.1; -; mRNA.
 DR EMBL; X69141; CAA48896.1; -; mRNA.
 DR EMBL; S76822; AAB33404.1; -; mRNA.
 DR EMBL; BC003573; AAH03573.1; -; mRNA.
 DR EMBL; BC009251; AAH09251.1; -; mRNA.
 DR EMBL; BC029641; AAH29641.1; -; mRNA.
 DR PIR; A45998; A45998.
 DR PIR; I38245; I38245.
 DR PDB; 1ZFV; X-ray; A/B/C=35-370.
 DR EMBL; ENSG0000079459; Homo sapiens.
 DR HGNC; HGNC:3629; PDFT1.
 DR H-InvDB; HIX0007319; -.
 DR MIM; 184420; -.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0006684; P:steroid biosynthesis; TAS.
 DR InterPro; IPR002060; Sgu/phyt_synthee.
 DR InterPro; IPR006449; Squal_synth.
 DR Pfam; PF00494; SQS_PSY; 1.
 DR TIGRFAMs; TIGR01559; squal_synth; 1.
 DR PROSITE; PS01044; SQUALEN_PHTOEN_SYN_2; 1.
 DR PROSITE; PS01045; SQUALEN_PHTOEN_SYN_1; 1.
 DR 3D-structure; Cholesterol biosynthesis; Endoplasmic reticulum;
 KM Isoenzyme biosynthesis; Lipid synthesis; Magnesium;
 KM Multifunctional enzyme; NADP; Oxidoreductase; Polymorphism;
 KM Steroid biosynthesis; Sterol biosynthesis; Transferase; Transmembrane.

FT	TRANSMEM	284	304	Potential.
FT	TRANSMEM	384	404	Potential.
FT	VARIANT	45	45	K -> R (in dbSNP:1047695) .
FT	VARIANT	392	392	/FTID=VAR_011786.
FT	VARIANT	392	392	L -> P (in dbSNP:1804473) .
FT	CONFLICT	353	353	/FTID=VAR_011787.
FT	CONFLICT	402	402	D -> N (in Ref. 4) .
FT	HELIX	39	50	T -> A (in Ref. 3) .
FT	HELIX	54	59	
FT	HELIX	60	60	
FT	TURN	63	63	
FT	HELIX	64	84	
FT	TURN	86	87	
FT	HELIX	90	103	
FT	TURN	104	105	
FT	TURN	107	108	
FT	TURN	117	118	
FT	HELIX	119	123	
FT	TURN	124	124	
FT	HELIX	125	133	
FT	TURN	134	134	
FT	HELIX	137	158	
FT	TURN	159	159	
FT	HELIX	165	175	
FT	TURN	176	176	
FT	HELIX	177	190	
FT	HELIX	191	191	
FT	HELIX	195	199	
FT	HELIX	201	218	
FT	TURN	219	219	
FT	HELIX	220	226	
FT	TURN	227	227	
FT	HELIX	233	236	
FT	TURN	237	239	
FT	HELIX	243	247	
FT	HELIX	249	251	
FT	HELIX	252	267	
FT	TURN	268	269	
FT	HELIX	270	278	
FT	TURN	279	279	
FT	HELIX	283	303	
FT	TURN	304	305	
FT	HELIX	310	310	
FT	TURN	311	311	
FT	TURN	328	329	
FT	HELIX	331	348	
FT	TURN	351	352	
FT	TURN	354	355	
FT	HELIX	356	367	
FT	TURN	368	368	
SO	SEQUENCE	417 AA;	48115 MW;	D36CB8382FE827EC CRC64;
Query Match	98.4%;	Score 1920.5;	DB 1;	Length 417;
Best Local Similarity	89.7%;	Pred. No. 8.2e-153;		
Matches 374;	Conservative	0;	Mismatches 0;	Indels 43; Gaps 1;
QY	1	MEFVKCLGHEEYVYVFRIGKRVKMPKMDODSSLSKTCYKTLNOTSRSFAVIOA	60	
DB	1	MEFVKCLGHEEYVYVFRIGKRVKMPKMDODSSLSKTCYKTLNOTSRSFAVIOA	60	
QY	61	LDGEMNAVCIFFLVLRALDTLEDWTISVEKKVPLLNHFSFLYQPDWRFMSKSKDRQ	120	
DB	61	LDGEMNAVCIFFLVLRALDTLEDWTISVEKKVPLLNHFSFLYQPDWRFMSKSKDRQ	120	
QY	121	VLEDFFPT-----YCHYVAGLVG	137	
DB	121	VLEDFFPT-----YCHYVAGLVG	137	
QY	138	IGISRLFSASEFPDPLVGDTERANSMGLFLOKTNIRDYLEDQGGREFWPEVWSRYV	197	
DB	181	IGISRLFSASEFPDPLVGDTERANSMGLFLOKTNIRDYLEDQGGREFWPEVWSRYV	240	

OY		125	PFTCHVAVAGLVIGLSTLSFASFEEDPLVGSDTRANSMGLFKOTNTIRLYLEDOGG	184
Db		131	TLRVCYHVAAGVLMMQAQMGVRD-----NATLDPADCLGAFOLTNARIIVDDAHNG	184
OY		185	REFWQEWSRVKXKLGDFAKPENIDLVAOCINELITNALHHIPDVITYLSRLRNSOVFN	244
Db		185	RCLYPASVLEHGLENKENYAAPENROALSRIARLVQGEPEP-----YLS-----ATAG	233
OY		245	FCAIPI--GVMAIATLAACYNNOVFKGAVKIRK--GOAVTLMMDATNMP	289
Db		234	LAGEPLRSAMAIATAKAQVTR-----KIGVKVEAQGAQADROSITTP	276
 RESULT 2*				
		US-10-524-972-116		
		; Sequence 116, Application US/10524972		
		; Publication No. US20060031963A1		
		GENERAL INFORMATION:		
		APPLICANT: Schopfer, Christel R.		
		APPLICANT: Flachmann, Ralf		
		APPLICANT: Herbers, Karin		
		APPLICANT: Kunze, Irene		
		APPLICANT: Sauer, Marc		
		APPLICANT: Klebsattel, Martin		
		TITLE OF INVENTION: Method for the production of Astaxanthin in flowers of plants		
		FILE REFERENCE: 13173-00007-US		
		CURRENT APPLICATION NUMBER: US/10/524, 972		
		CURRENT FILING DATE: 2005-02-18		
		PRIOR APPLICATION NUMBER: PCT/EP2003/009102		
		PRIOR FILING DATE: 2003-08-18		
		PRIOR APPLICATION NUMBER: DE 102 38 980.2		
		PRIOR FILING DATE: 2002-08-20		
		PRIOR APPLICATION NUMBER: DE 102 38 978.0		
		PRIOR FILING DATE: 2002-08-20		
		PRIOR APPLICATION NUMBER: DE 102 38 979.9		
		PRIOR FILING DATE: 2002-08-20		
		PRIOR APPLICATION NUMBER: DE 102 53 112.9		
		PRIOR FILING DATE: 2002-11-13		
		PRIOR APPLICATION NUMBER: DE 102 58 971.2		
		PRIOR FILING DATE: 2002-12-16		
		NUMBER OF SEQ ID NOS: 172		
		SOFTWARE: PatentIn version 3.3		
		SEQ ID NO 116		
		LENGTH: 309		
		TYPE: PR1		
		ORGANISM: Erwinia uredovora		
		US-10-524-972-116		
		Query Match	9.3%; Score 181; DB 6; Length 309;	
		Best Local Similarity	22.9%; Pred. No. 4, 7e-09;	
		Matches	66; Conservative 37; Mismatches 107; Indels 78; Gaps 8;	
OY		51	SRSFAAVIQALDGEMRNACIFYLVLRALEDTEDDMTISVEKKVPLLNHFHSFLVPDR	110
Db		18	SKSFPTASKLFPAKTRSVLMLYAWCRHCDVIDDTLGFGARQPALQT-----PEGR	70
OY		111	FMSSEKROV-----	124
Db		71	LMQLEMKTROAVAGSQMHPAPAFOEVAMANDIAPAYAFDHLEBGRAMDYREAOYSQLDD	130
OY		125	PPTYCHVAVAGLVIGLSRLFSASEEDPLVGSDTERANSMDLFLOXTNIIRDYLEDOGG	184
Db		131	TLRVCYHVAAGVLMMQAQMGVRD-----NATLDPADCLGAFOLTNARIIVDDAHNG	184
OY		185	REFWQEWSRVKXKLGDFAKPENIDLVAOCINELITNALHHIPDVITYLSRLRNSOVFN	244
Db		185	RCLYPASVLEHGLENKENYAAPENROALSRIARLVQGEPEP-----YLS-----ATAG	233
OY		245	FCAIPI--GVMAIATLAACYNNOVFKGAVKIRK--GOAVTLMMDATNMP	289
Db		234	LAGEPLRSAMAIATAKAQVTR-----KIGVKVEAQGAQADROSITTP	276

```

RESULT 3
US-10-467-657-5128
; Sequence 5128, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIIGNANI Vega
; APPLICANT: MONACT Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 5128
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5128

Query Match      8.2%; Score 159.5; DB 6; Length 290;
Best Local Similarity 23.6%; Pred. No. 4,2e-07;
Matches 78; Conservative 40; Mismatches 106; Indels 107; Gaps 12;

QY      40 LKTYKYLNQTSRSPAAVIAIQALDGENRNAVCIFYLVLRALDPTLEDMTISVEKKVPL--- 96
DB      4 LDYCRQKAESRSSTLSGFRFLTOEKODAVTVLYAFCEHLDVDECSNDVQAATLNMW 63
QY      97 -----LNFPSFLYQOPWRFMESKEKQKQVL-----EDPEPTY 128
DB      64 RGLDLNAGMAMPBEPVNOALQVKETFKLPYTELEALIDGMQMDLYQARYSGFEELKLY 123
QY      129 CHYVAGLVGIGLSRLFSASEFEDPLVGEDTERANSGLFLQKTNIIIRDYLEDOQGGEFW 188
DB      124 CRVAGVGVGCLIAIRLIGFSD-----GKTLVEADKKGVALQLTNIIRDVGEDARGRHLY 177
QY      189 PQEWSRVRVKKLGDPAKEPNIDLAVOCLNELITNALHHPDVITYYSRLRNQSVNFCAI 248
DB      178 PMEWQR-----PDVPASVTL--QC-----SPTGNA-- 202
QY      249 PQWAIATLAACYNNOQVFEKGAVKI-----RKGAATLMMDATNMPAVKAIITYQMEIY 303
DB      203 -ELWAFQIKRA---RETYREAVSLIPDADKCAQKQGLVW-----AAVYTAALLNEI- 248
QY      304 HRIPDSD-----PSSSKTRQIIST 322
DB      249 ----DRDGAQNVLYKKYKIALPSPRKKRIALKT 275

RESULT 4
US-11-096-568A-6786
; Sequence 6786, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6786
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(399)

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OM protein - protein search, using sw model

Run on: March 24, 2006, 16:46:05 ; Search time 40 Seconds
(without alignments)
899.627 Million cell updates/sec

Title: US-10-644-021A-2

Perfect score: 1952
Sequence: 1 MEVFKCLGHPPEEFLVLRFR.....WQVLTTLSTQVTEDEVQNGE 374

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_80:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1920.5	98.4	417	2	A45998
2	1915.5	98.1	417	2	I38245
3	1912.5	98.0	417	2	I52090
4	1737	89.0	416	2	S52075
5	1692	86.7	416	2	A45105
6	749.5	38.4	401	2	T00489
7	746.5	38.2	411	2	S71771
8	744	38.1	460	2	B48057
9	744	38.1	460	2	T40581
10	736	37.7	413	2	E65408
11	732	37.5	413	2	T44924
12	731.5	37.5	413	2	T05262
13	731	37.4	410	2	S54251
14	729	37.3	412	2	JCS031
15	720.5	36.9	413	2	JCS030
16	688.5	35.3	444	1	S46682
17	652.5	33.4	412	2	T05285
18	603	30.9	376	2	T02167
19	202	10.3	277	2	S75973
20	181	9.3	296	2	E37802
21	181	9.3	390	2	A84226
22	171	8.8	296	2	S52587
23	168.5	8.6	290	2	A81118
24	166	8.5	287	2	AG2031
25	165.5	8.5	362	2	T45141
26	160.5	8.2	290	2	H81902
27	145	7.4	287	2	C90061
28	143.5	7.4	307	2	S20383
29	138.5	7.1	309	2	B39273

30	134.5	6.9	312	2	T35400	probable phytoene
31	125	6.4	254	2	A55548	crtm protein - Sta
32	121.5	6.2	337	2	S45360	phytoene synthase
33	116	5.9	410	2	S68307	phytoene synthase
34	112	5.7	310	2	AC2035	phytoene synthase
35	112	5.7	325	2	D75466	phytoene synthase
36	112	5.7	602	2	A53583	geranylgeranyl-dip
37	111	5.7	344	2	T50895	prephytoene pyroph
38	111	5.7	412	2	A42102	phytoene synthase
39	111	5.7	412	2	S22474	phytoene synthase
40	110	5.6	336	2	S32170	phytoene synthetas
41	109	5.6	423	2	S54135	phytoene synthase
42	108	5.5	1351	2	E97273	superfamily I DNA
43	107	5.5	310	2	A49558	phytoene synthase
44	103.5	5.3	316	2	H89995	sucrose operon rep
45	100.5	5.1	315	2	C82425	sensor histidine kin

ALIGNMENTS

```
RESULT 1
A45998
farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) - human
N:Alternate names: squalene synthase
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A45998; A46057
R:Jiang, G.; McKenzie, T.L.; Conrad, D.G.; Shechter, I.
J. Biol. Chem. 268, 12818-12824, 1993
A:Title: Transcriptional regulation by lovastatin and 25-hydroxycholesterol in HepG2 cell
A:Reference number: A45998; MUID:93266128; PMID:7685352
A:Accession: A45998
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-417 <JIA>
A:Cross-references: UNIPROT:P37268; UNIPARC:UPI000012A5D5; GB:L06105; NID:G307431; PIDN:J
A:Experimental source: hepatoma cell line HepG2
R:Robinson, G.W.; Terry, Y.H.; Kienzie, B.K.; Smith-Monroy, C.A.; Bishop, R.W.
Mol. Cell. Biol. 13, 2706-2717, 1993
A:Title: Conservation between human and fungal squalene synthetases: similarities in str
A:Reference number: A48057; MUID:93233634; PMID:8474436
A:Accession: A48057
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-417 <ROB>
A:Cross-references: UNIPARC:UPI000012A5D5; GB:L06070; NID:G292509; PIDN:AAA60582.1; PID:G
C:Superfamily: farnesyl-diphosphate farnesyltransferase
C:Keywords: transference; transmembrane protein
Query Match 98.4%; Score 1920.5; DB 2; Length 417;
Best Local Similarity 89.7%; Pred. No. 7.4e-148;
Matches 374; Conservative 0; Mismatches 0; Indels 43; Gaps 1;
OY 1 MEVFKCLGHPPEEFLVLRFRIGGRKMPKMDQSSLSLTKCYKYNQNSRSPAAYIA 60
DB 1 MEVFKCLGHPPEEFLVLRFRIGGRKMPKMDQSSLSLTKCYKYNQNSRSPAAYIA 60
OY 1 LDGEMRNANVCIFYVLRALDTLEDMDTISYEKKVPLAHNFSPFYOPDMRPMESKEDRQ 120
DB 1 LDGEMRNANVCIFYVLRALDTLEDMDTISYEKKVPLAHNFSPFYOPDMRPMESKEDRQ 120
OY 121 VLDEFPPT-----YCHYVAAGLVG 137
DB 121 VLDEFPPTISLEFRNLAEKYQTIVADICRMGIGMAEFLDKHVTSEQEWMKCYCHYVAGLVG 180
OY 138 IGLSRLPSASFEEDPLVGEDTERANSGLFLQKNTIIRDYLEDQGGREFPQSVWRRYV 197
DB 181 IGLSRLPSASFEEDPLVGEDTERANSGLFLQKNTIIRDYLEDQGGREFPQSVWRRYV 240
OY 198 KKLDDFAKPEINIDLAVQCLNBLINLALHHPDIVTYSRLANGSVFNFCALPQWAIATL 257
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Db 241 KKLGDFAKPEINIDLAQCINELITNALHHIPDVITYLSRLNOSVFNFCAIPQVMAIATL 300
|||
Qy 258 AACNNQOVFKGAVKIRKGOAVTLMMDATNMPAKAIITYQMEIYHRIIDSPSSSKTR 317
|||
Db 301 AACNNQOVFKGAVKIRKGOAVTLMMDATNMPAKAIITYQMEIYHRIIDSPSSSKTR 360
|||
Qy 318 QIISTIRTONLPNCOLISRSRHSPIYLSFVWLLAALSMQYLTTLTSLQVTEDEVQGTGH 374
|||
Db 361 QIISTIRTONLPNCOLISRSRHSPIYLSFVWLLAALSMQYLTTLTSLQVTEDEVQGTGH 417
|||

RESULT 2
138245
farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21), hepatic - human
N:Alternate names: squalene synthase
C:Species: Homo sapiens (man)
C>Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004
C:Accession: I38245
R:Summers, C.; Karst, F.; Charles, A.D.
Gene 136, 185-192, 1993
A:Title: Cloning, expression and characterization of the cDNA encoding human hepatic sq
A:Reference number: I38245; MUID:94123956; PMID:8294001
A:Accession: I38245
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-417 <RES>
A:Cross-references: UNIPROT:P37268; UNIPARC:UPI0000168067; EMBL:X69141; NID:9435676; PID
C:Superfamily: farnesyl-diphosphate farnesyltransferase
C:Keywords: liver; membrane protein; steroid biosynthesis; transferase

Query Match 98.1%; Score 1915.5; DB 2; Length 417;
Best Local Similarity 89.4%; Pred. No. 1.9e-147;
Matches 373; Conservative 0; Mismatches 1; Indels 43; Gaps 1;

Qy 1 MEFVKCLGHPPEEYNLVRRIGGRKVMKMDODSLSSSLKTCYKYLNTGSRFAVIOA 60
|||
Db 1 MEFVKCLGHPPEEYNLVRRIGGRKVMKMDODSLSSSLKTCYKYLNTGSRFAVIOA 60
|||
Qy 61 LDGEMNNAVCIFYLVLRALDTEEDMTISVEKKVPLLNHPSFLYQPDWRFMSKSKDRQ 120
|||
Db 61 LDGEMNNAVCIFYLVLRALDTEEDMTISVEKKVPLLNHPSFLYQPDWRFMSKSKDRQ 120
|||
Qy 121 VLDEPFT-----YCHYVAGLVG 137
|||
Db 121 VLDEPFTISLEFRNLAEKYQTVIADICRMGIGMAEFLDKHTVSEQWMDKCHYVAGLVG 180
|||
Qy 138 IGLSRLFSASEFEDPLVGEDTERANSMLFLQKTNIIIRDYLEDOQGRFEPQEWMSRYV 197
|||
Db 181 IGLSRLFSASEFEDPLVGEDTERANSMLFLQKTNIIIRDYLEDOQGRFEPQEWMSRYV 240
|||
Qy 198 KKLGDFAKPEINIDLAQCINELITNALHHIPDVITYLSRLNOSVFNFCAIPQVMAIATL 257
|||
Db 241 KKLGDFAKPEINIDLAQCINELITNALHHIPDVITYLSRLNOSVFNFCAIPQVMAIATL 300
|||
Qy 258 AACNNQOVFKGAVKIRKGOAVTLMMDATNMPAKAIITYQMEIYHRIIDSPSSSKTR 317
|||
Db 301 AACNNQOVFKGAVKIRKGOAVTLMMDATNMPAKAIITYQMEIYHRIIDSPSSSKTR 360
|||
Qy 318 QIISTIRTONLPNCOLISRSRHSPIYLSFVWLLAALSMQYLTTLTSLQVTEDEVQGTGH 374
|||
Db 361 QIISTIRTONLPNCOLISRSRHSPIYLSFVWLLAALSMQYLTTLTSLQVTEDEVQGTGH 417
|||

RESULT 3
152090
squalene synthase - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C:Accession: I52090
R:Solite, D.A.; McMahon, G.; Caplan, S.L.; Duda, D.A.; Chamberlin, H.A.; Vattay, A.; Do
Arch. Biochem. Biophys. 316, 713-723, 1995
A:Title: Expression, purification, and characterization of the human squalene synthase:

A:Reference number: I52090; MUID:95168856; PMID:7864626
A:Accession: I52090
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-417 <RES>
A:Cross-references: UNIPARC:UPI000016847A; GB:S76822; NID:9413348; PIDN:AA83404.1; PID:C
C:Superfamily: farnesyl-diphosphate farnesyltransferase

Query Match 98.0%; Score 1912.5; DB 2; Length 417;
Best Local Similarity 89.2%; Pred. No. 3.3e-147;
Matches 372; Conservative 2; Mismatches 0; Indels 43; Gaps 1;

Qy 1 MEFVKCLGHPPEEYNLVRRIGGRKVMKMDODSLSSSLKTCYKYLNTGSRFAVIOA 60
|||
Db 1 MEFVKCLGHPPEEYNLVRRIGGRKVMKMDODSLSSSLKTCYKYLNTGSRFAVIOA 60
|||
Qy 61 LDGEMNNAVCIFYLVLRALDTEEDMTISVEKKVPLLNHPSFLYQPDWRFMSKSKDRQ 120
|||
Db 61 LDGEMNNAVCIFYLVLRALDTEEDMTISVEKKVPLLNHPSFLYQPDWRFMSKSKDRQ 120
|||
Qy 121 VLDEPFT-----YCHYVAGLVG 137
|||
Db 121 VLDEPFTISLEFRNLAEKYQTVIADICRMGIGMAEFLDKHTVSEQWMDKCHYVAGLVG 180
|||
Qy 138 IGLSRLFSASEFEDPLVGEDTERANSMLFLQKTNIIIRDYLEDOQGRFEPQEWMSRYV 197
|||
Db 181 IGLSRLFSASEFEDPLVGEDTERANSMLFLQKTNIIIRDYLEDOQGRFEPQEWMSRYV 240
|||
Qy 198 KKLGDFAKPEINIDLAQCINELITNALHHIPDVITYLSRLNOSVFNFCAIPQVMAIATL 257
|||
Db 241 KKLGDFAKPEINIDLAQCINELITNALHHIPDVITYLSRLNOSVFNFCAIPQVMAIATL 300
|||
Qy 258 AACNNQOVFKGAVKIRKGOAVTLMMDATNMPAKAIITYQMEIYHRIIDSPSSSKTR 317
|||
Db 301 AACNNQOVFKGAVKIRKGOAVTLMMDATNMPAKAIITYQMEIYHRIIDSPSSSKTR 360
|||
Qy 318 QIISTIRTONLPNCOLISRSRHSPIYLSFVWLLAALSMQYLTTLTSLQVTEDEVQGTGH 374
|||
Db 361 QIISTIRTONLPNCOLISRSRHSPIYLSFVWLLAALSMQYLTTLTSLQVTEDEVQGTGH 417
|||

RESULT 4
S52075
farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) - mouse
N:Alternate names: squalene synthase
C:Species: Mus musculus (house mouse)
C>Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S52075
R:Inoue, T.; Osuni, T.; Hata, S.
Biochim. Biophys. Acta 1260, 49-54, 1995
A:Title: Molecular cloning and functional expression of a cDNA for mouse squalene synthet
A:Reference number: S52075; MUID:95092793; PMID:7999794
A:Accession: S52075
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-416 <INO>
A:Cross-references: UNIPROT:P53798; UNIPARC:UPI000029C34; EMBL:D29016; NID:9468456; PID
C:Superfamily: farnesyl-diphosphate farnesyltransferase
C:Keywords: transferase

Query Match 89.0%; Score 1737; DB 2; Length 416;
Best Local Similarity 79.6%; Pred. No. 5.5e-133;
Matches 337; Conservative 26; Mismatches 15; Indels 44; Gaps 2;

Qy 1 MEFVKCLGHPPEEYNLVRRIGGRKVMKMDODSLSSSLKTCYKYLNTGSRFAVIOA 60
|||
Db 1 MEFVKCLGHPPEEYNLVRRIGGRKVMKMDODSLSSSLKTCYKYLNTGSRFAVIOA 60
|||
Qy 61 LDGEMNNAVCIFYLVLRALDTEEDMTISVEKKVPLLNHPSFLYQPDWRFMSKSKDRQ 120
|||
Db 61 LDGEMNNAVCIFYLVLRALDTEEDMTISVEKKVPLLNHPSFLYQPDWRFMSKSKDRQ 120
|||
Qy 121 VLDEPFT-----YCHYVAGLVG 137
|||

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OM protein - protein search, using sw model

Run on: March 24, 2006, 17:01:21 ; Search time 166 Seconds
(Without alignments)
941.375 Million cell updates/sec

Title: US-10-644-021A-2

Perfect score: 1952
1 MEFVCKLGHPEEFYNLVRRF.....WOYLTLSQVTEEDYVOTGEH 374

Scoring table: BL0SUM62
Gapop 10.0 , Gapect 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications_AA_Main:*

- 1: /cgn2_6/ptcdatc/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptcdatc/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptcdatc/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptcdatc/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptcdatc/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptcdatc/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1952	100.0	374	3	US-09-820-004-2
2	1952	100.0	374	4	US-10-644-021A-2
3	1920.5	98.4	417	3	US-09-820-004-4
4	1920.5	98.4	417	3	US-09-820-004-5
5	1920.5	98.4	417	4	US-X0-287-226-100
6	1920.5	98.4	417	4	US-10-644-021A-4
7	1920.5	98.4	417	4	US-10-644-021A-5
8	1915.5	98.1	417	3	US-09-820-004-6
9	1915.5	98.1	417	3	US-10-644-021A-6
10	1692	86.7	416	4	US-10-205-194-67
11	770.5	39.5	455	4	US-10-425-114-66845
12	759.5	38.9	403	4	US-10-425-115-221234
13	753.5	38.6	403	4	US-10-437-963-187558
14	747.5	38.3	401	4	US-10-425-115-222973
15	744	38.1	460	4	US-10-369-493-2381
16	735.5	37.7	428	4	US-10-425-114-66845
17	732	37.5	404	5	US-10-739-930-10172
18	731	37.4	410	4	US-10-024-130A-2
19	723.5	37.1	448	4	US-10-033-585-7355
20	717.5	36.8	413	4	US-10-423-949-5
21	716.5	36.7	388	4	US-10-024-130A-6
22	706.5	36.2	328	4	US-10-424-599-255117
23	695.5	35.6	528	4	US-10-128-714-8505
24	688.5	35.3	444	4	US-10-369-493-22063
25	685	35.1	520	4	US-10-128-714-3505
26	676	34.6	354	4	US-10-369-493-12039
27	660.5	33.8	388	4	US-10-425-114-66893

28	656.5	33.6	410	4	US-10-259-194A-170	Sequence 170, App
29	652.5	33.4	445	4	US-10-425-115-221233	Sequence 221233,
30	651	33.4	356	4	US-10-369-493-3321	Sequence 3321, Ap
31	584	29.9	469	4	US-10-437-963-202945	Sequence 202945,
32	564	28.9	249	4	US-10-425-114-44936	Sequence 44936, A
33	533	27.3	283	4	US-10-425-115-203778	Sequence 49024, A
34	391	20.0	223	4	US-10-425-115-203778	Sequence 203778,
35	391	20.0	239	4	US-10-425-115-203778	Sequence 306328,
36	354	18.1	231	4	US-10-425-114-43038	Sequence 43038, A
37	345.5	17.7	122	4	US-10-767-701-49986	Sequence 49986, A
38	306	15.7	158	4	US-10-425-114-52931	Sequence 52931, A
39	271.5	13.9	175	4	US-10-767-701-41758	Sequence 41758, A
40	244	12.5	225	4	US-10-038-854-133	Sequence 133, App
41	243	12.4	120	4	US-10-425-115-287994	Sequence 287994,
42	210	10.8	363	4	US-10-358-917-2	Sequence 2, Appl1
43	210	10.8	363	5	US-10-860-291-2	Sequence 2, Appl1
44	199.5	10.2	112	4	US-10-424-599-236999	Sequence 236999,
45	181	9.3	390	4	US-10-369-493-18574	Sequence 18574, A

ALIGNMENTS

RESULT 1									
US-09-820-004-2									
; Sequence 2, Application US/09820004									
; Patent No. US20020142418A1									
; GENERAL INFORMATION:									
; APPLICANT: WEI, Ming-Hui et al.									
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC									
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES									
; FILE REFERENCE: C1001201									
; CURRENT APPLICATION NUMBER: US/09/820,004									
; NUMBER OF SEQ ID NOS: 6									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 2									
; LENGTH: 374									
; TYPE: PRT									
; ORGANISM: Human									
US-09-820-004-2									
Query Match									
Best Local Similarity 100.0%; Pred. No. 2.6e-187; Length 374;									
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MEFYCKLGHPEEFYNLVRRFIRIGGRKVMKMDQSSLSKTCYKYNQTSRSPAVIQ	60						
DB	1	MEFYCKLGHPEEFYNLVRRFIRIGGRKVMKMDQSSLSKTCYKYNQTSRSPAVIQ	60						
QY	61	LDGEMRNAVCIFYLVRLADLTLEDMTISVEKKVPLLNHFSFLYQDMRPMESKEDRQ	120						
DB	61	LDGEMRNAVCIFYLVRLADLTLEDMTISVEKKVPLLNHFSFLYQDMRPMESKEDRQ	120						
QY	121	VLEPFPTCYHVAIGVIGSRFLFSASEFEDPLVGEDETERANSGLQKNTIIRDYLED	180						
DB	121	VLEPFPTCYHVAIGVIGSRFLFSASEFEDPLVGEDETERANSGLQKNTIIRDYLED	180						
QY	181	QGGREPMPOEVMRSYKKGDFAKPENIDLAQCINELITNALHHPDVTIYLSRLNQ	240						
DB	181	QGGREPMPOEVMRSYKKGDFAKPENIDLAQCINELITNALHHPDVTIYLSRLNQ	240						
QY	241	SVNFCAIPQVMAIATLAACYNQOVFGKAVIRKGAQVILMDATMPAVKAIITYOME	300						
DB	241	SVNFCAIPQVMAIATLAACYNQOVFGKAVIRKGAQVILMDATMPAVKAIITYOME	300						
QY	301	EYHRIQSDPSSSKTQIISTITFTQNLPCQILSRSHSPITYLSFVMLAASMOYLT	360						
DB	301	EYHRIQSDPSSSKTQIISTITFTQNLPCQILSRSHSPITYLSFVMLAASMOYLT	360						
QY	361	LSQVTEEDYVOTGEH 374							
DB	361	LSQVTEEDYVOTGEH 374							

Db 361 LSGVTEBDYVQTGEH 374

RESULT 2

US-10-644-021A-2
; Sequence 2, Application US/10644021A
; Publication No. US20040106179A1
; GENERAL INFORMATION:

APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
FILE OF INVENTION: THEREOF

FILE REFERENCE: CL001201DI
CURRENT APPLICATION NUMBER: US/10/644,021A
CURRENT FILING DATE: 2003-08-20
PRIOR APPLICATION NUMBER: 09/820,004
PRIOR FILING DATE: 03-29-2001

NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 374

TYPE: PRT

ORGANISM: Human

US-10-644-021A-2

Query Match 100.0%; Score 1952; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 2, 6e-187;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEVFKCLGHPBEFYNLVRRIGGRKVMKMDODSLSSSLKTCYKYNQTSRSPAIVQA 60

Db 1 MEVFKCLGHPBEFYNLVRRIGGRKVMKMDODSLSSSLKTCYKYNQTSRSPAIVQA 60

QY 61 LDGEMNAVCIFYLVLRALDLEDDMTISVEKKVPLLNHNSFLYOPDMRFMESKEKDRQ 120

Db 61 LDGEMNAVCIFYLVLRALDLEDDMTISVEKKVPLLNHNSFLYOPDMRFMESKEKDRQ 120

QY 121 VLEDPTTISLEFRNLAEKYQTVIADI CRRMGIGMAEFLDKHVTSEQEMDKYCHYVAGLVG 180

Db 121 VLEDPTTISLEFRNLAEKYQTVIADI CRRMGIGMAEFLDKHVTSEQEMDKYCHYVAGLVG 180

QY 181 QGGREFEPOEWSRYYKLGDFAKPENIDLAOCINELITNALHHIPDVTYLSRLNRQ 240

Db 181 QGGREFEPOEWSRYYKLGDFAKPENIDLAOCINELITNALHHIPDVTYLSRLNRQ 240

QY 241 SVNFPCAIPQVMAIATLAAACYNNOQVFKGAVKIRKGOAVTLMDATMPAVKAIYQYME 300

Db 241 SVNFPCAIPQVMAIATLAAACYNNOQVFKGAVKIRKGOAVTLMDATMPAVKAIYQYME 300

QY 301 EIYHRIIDSPSSSKTRQIISTIRTONLPNCOLISRSRHSPIYLSFVMLAALSMQYLT 360

Db 301 EIYHRIIDSPSSSKTRQIISTIRTONLPNCOLISRSRHSPIYLSFVMLAALSMQYLT 360

QY 361 LSGVTEBDYVQTGEH 374

Db 361 LSGVTEBDYVQTGEH 374

RESULT 3

US-09-820-004-4
; Sequence 4, Application US/09820004
; Patent No. US20020142418A1
; GENERAL INFORMATION:

APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
FILE REFERENCE: CL001201
CURRENT APPLICATION NUMBER: US/09/820,004
CURRENT FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4

LENGTH: 417

TYPE: PRT

ORGANISM: Human

US-09-820-004-4

Query Match 98.4%; Score 1920.5; DB 3; Length 417;
Best Local Similarity 89.7%; Pred. No. 4, 5e-184;
Matches 374; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

QY 1 MEVFKCLGHPBEFYNLVRRIGGRKVMKMDODSLSSSLKTCYKYNQTSRSPAIVQA 60

Db 1 MEVFKCLGHPBEFYNLVRRIGGRKVMKMDODSLSSSLKTCYKYNQTSRSPAIVQA 60

QY 61 LDGEMNAVCIFYLVLRALDLEDDMTISVEKKVPLLNHNSFLYOPDMRFMESKEKDRQ 120

Db 61 LDGEMNAVCIFYLVLRALDLEDDMTISVEKKVPLLNHNSFLYOPDMRFMESKEKDRQ 120

QY 121 VLEDPTTISLEFRNLAEKYQTVIADI CRRMGIGMAEFLDKHVTSEQEMDKYCHYVAGLVG 137

Db 121 VLEDPTTISLEFRNLAEKYQTVIADI CRRMGIGMAEFLDKHVTSEQEMDKYCHYVAGLVG 180

QY 138 IGLSRIFSASEFEDPLVGEDTERANSMGLFLOKTNIIIPDYLEDQGGREFEPOEWSRYY 197

Db 181 IGLSRIFSASEFEDPLVGEDTERANSMGLFLOKTNIIIPDYLEDQGGREFEPOEWSRYY 240

QY 198 KKLGDPAKPEIDLAOCINELITNALHHIPDVTYLSRLNRQSVNFPCAIPQVMAIATL 257

Db 241 KKLGDPAKPEIDLAOCINELITNALHHIPDVTYLSRLNRQSVNFPCAIPQVMAIATL 300

QY 258 AACYNNOQVFKGAVKIRKGOAVTLMDATMPAVKAIYQYMEIYHRIIDSPSSSKTR 317

Db 301 AACYNNOQVFKGAVKIRKGOAVTLMDATMPAVKAIYQYMEIYHRIIDSPSSSKTR 360

QY 318 QIISTIRTONLPNCOLISRSRHSPIYLSFVMLAALSMQYLTLSGVTEBDYVQTGEH 374

Db 361 QIISTIRTONLPNCOLISRSRHSPIYLSFVMLAALSMQYLTLSGVTEBDYVQTGEH 417

RESULT 4

US-09-820-004-5
; Sequence 5, Application US/09820004
; Patent No. US20020142418A1
; GENERAL INFORMATION:

APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
FILE OF INVENTION: THEREOF

FILE REFERENCE: CL001201

CURRENT APPLICATION NUMBER: US/09/820,004

CURRENT FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 417

TYPE: PRT

ORGANISM: Human

US-09-820-004-5

Query Match 98.4%; Score 1920.5; DB 3; Length 417;
Best Local Similarity 89.7%; Pred. No. 4, 5e-184;
Matches 374; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

QY 1 MEVFKCLGHPBEFYNLVRRIGGRKVMKMDODSLSSSLKTCYKYNQTSRSPAIVQA 60

Db 1 MEVFKCLGHPBEFYNLVRRIGGRKVMKMDODSLSSSLKTCYKYNQTSRSPAIVQA 60

QY 61 LDGEMNAVCIFYLVLRALDLEDDMTISVEKKVPLLNHNSFLYOPDMRFMESKEKDRQ 120

Db 61 LDGEMNAVCIFYLVLRALDLEDDMTISVEKKVPLLNHNSFLYOPDMRFMESKEKDRQ 120

QY 121 VLEDPTTISLEFRNLAEKYQTVIADI CRRMGIGMAEFLDKHVTSEQEMDKYCHYVAGLVG 137

Db 121 VLEDPTTISLEFRNLAEKYQTVIADI CRRMGIGMAEFLDKHVTSEQEMDKYCHYVAGLVG 180